

Fig. 1

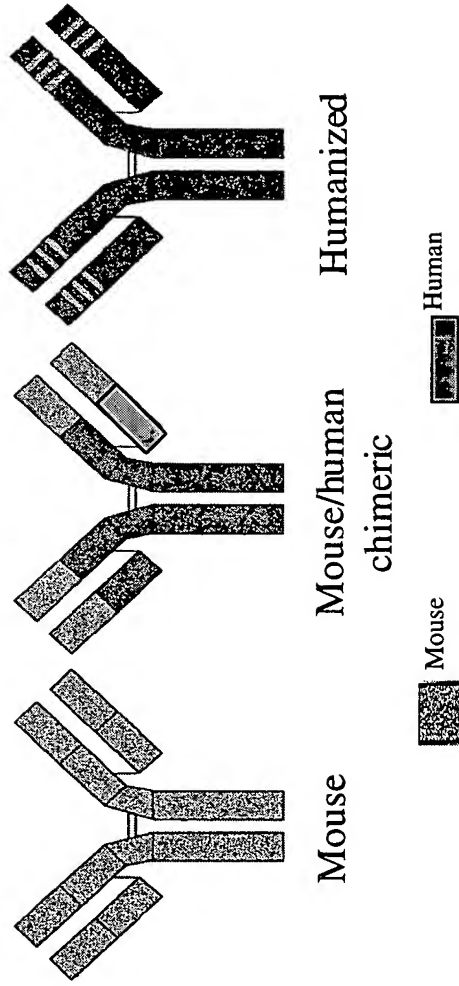


Fig. 2

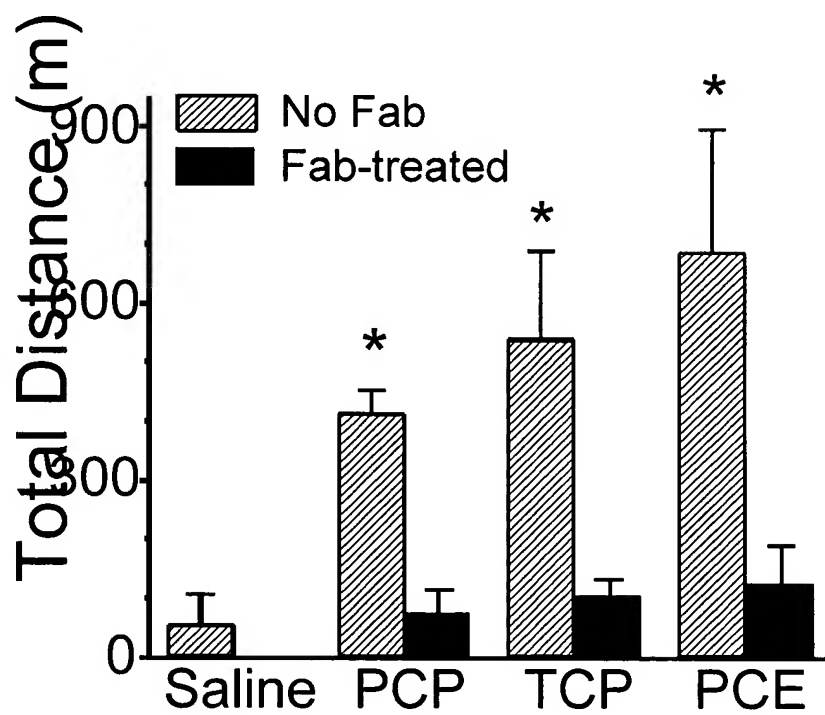
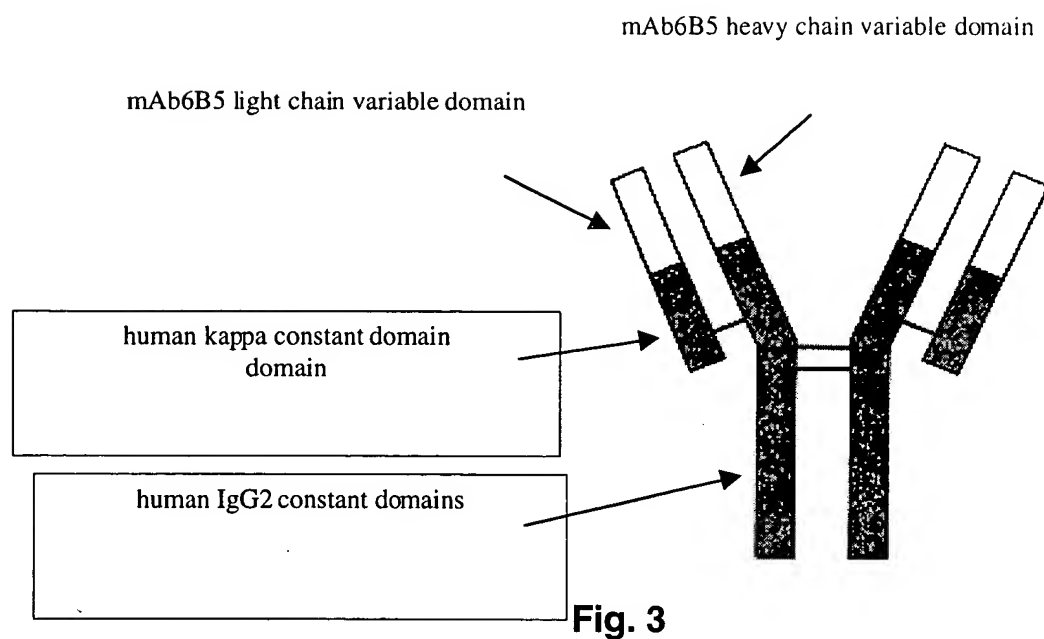


Fig. 4

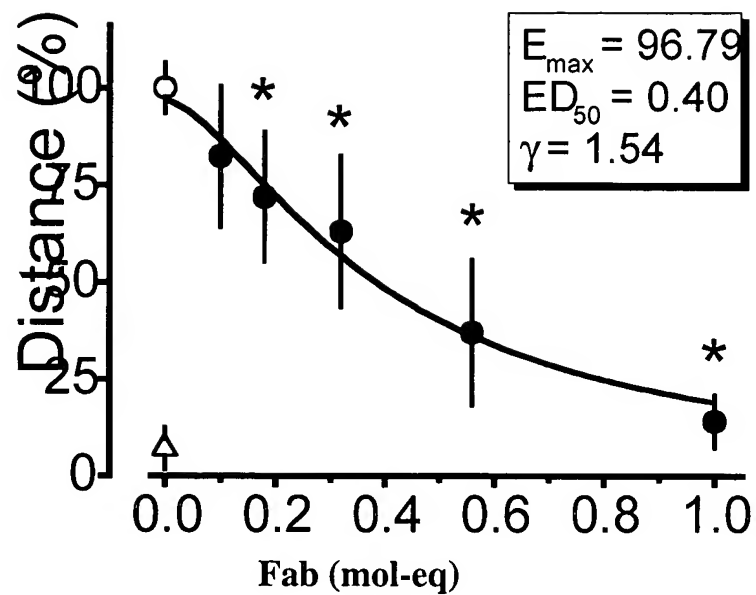


Fig. 5

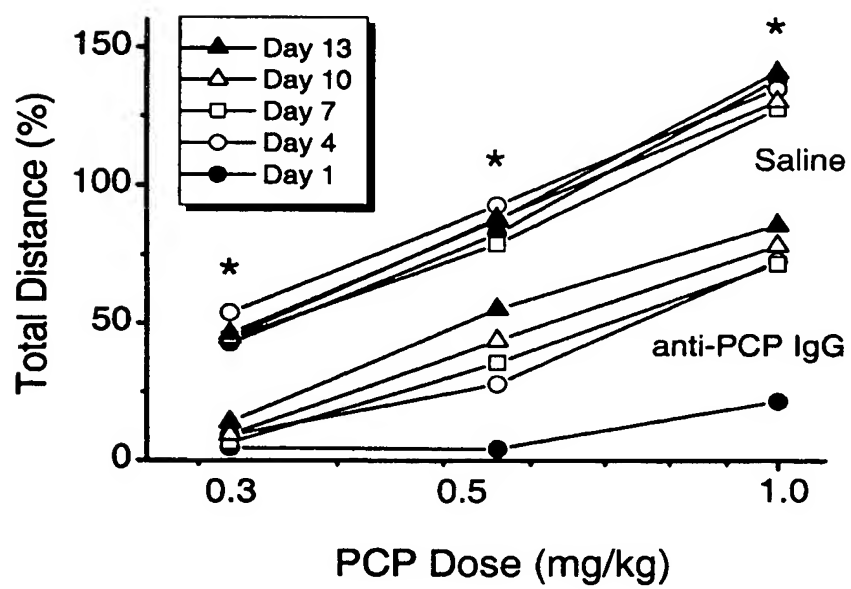


Fig. 6

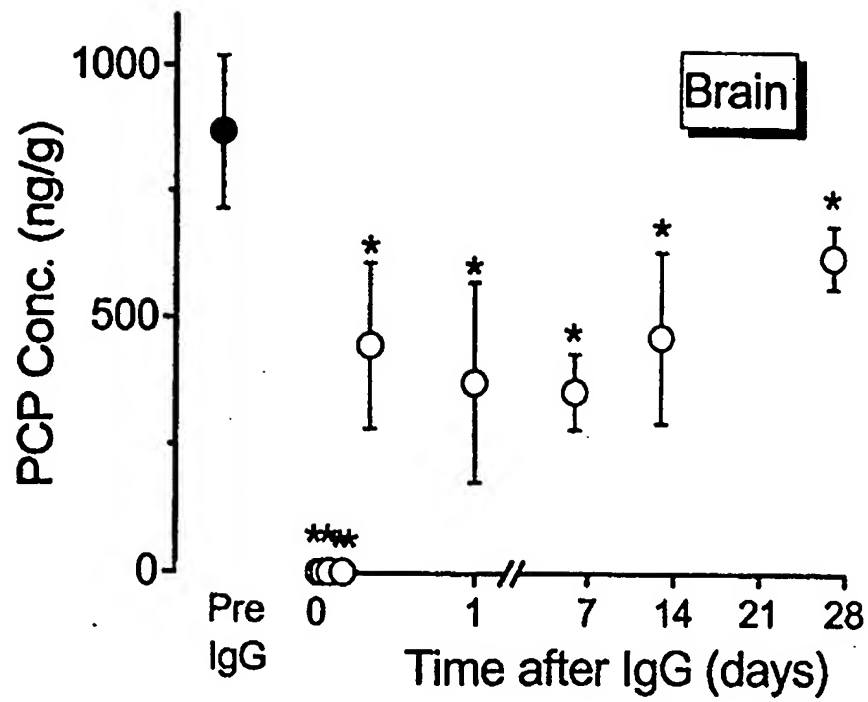


Fig. 7

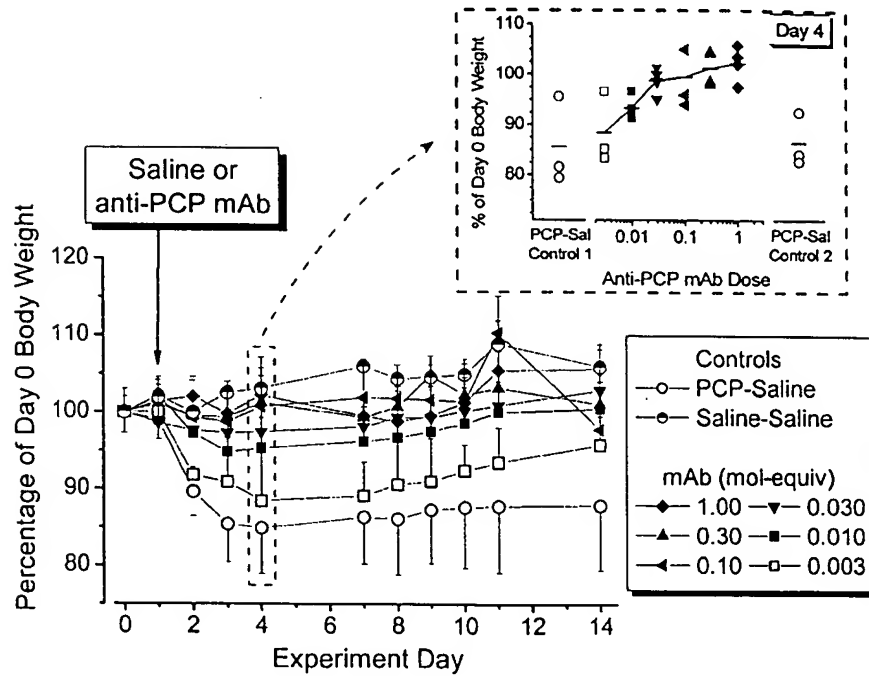


Fig. 8

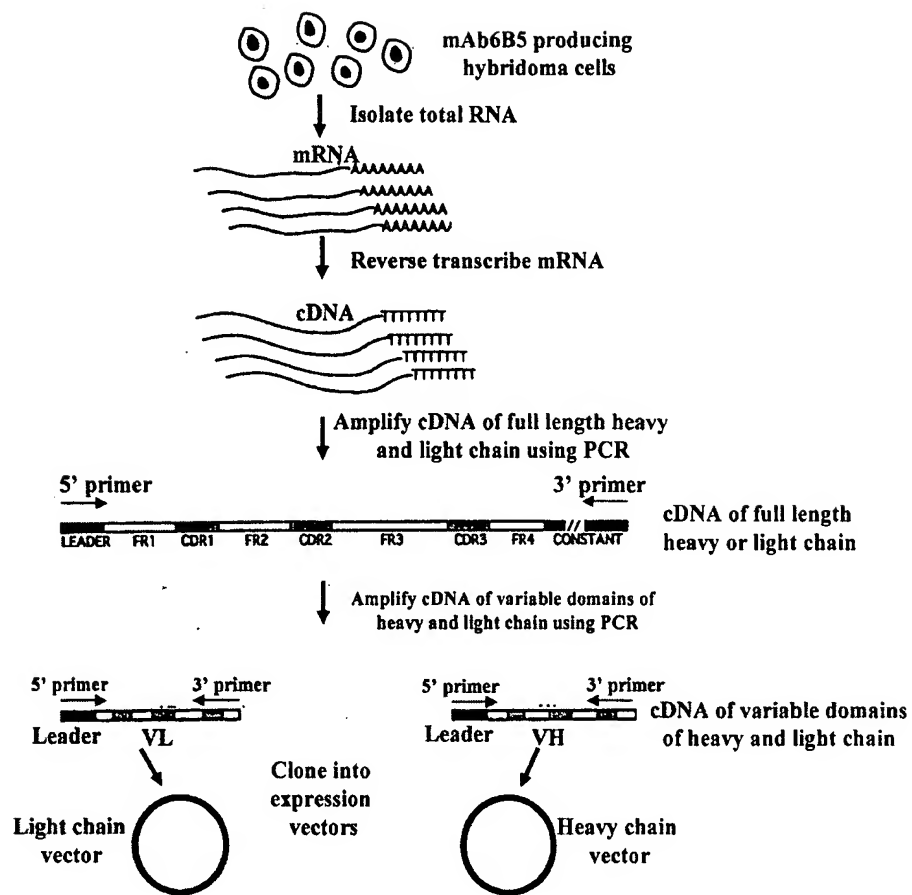


Fig. 9

1 - ATGAAGTTGCCCTGTAGGCTGTTGGTGCCTGATGTTCTGGATTCTCTGCTTCCAGCAGTGAT - 60
- M K L P V R L L V L M F W I P A S S D
61 - GTTTTGATGACCCAAACTCCACTCTCCCTGCCCTGTCAAGTCTTGGAGATCAAGCCTCCATC - 120
- V L M T Q T P L S L P V S L G D Q A S I
121 - TCTTGCAGATCTAGTCAGACCAATTGTACATAGTAATGGAACACACCTATTTAGAAATGGTAC - 180
- S C R S S Q T I V H S N G N T Y L E W Y
181 - CTGCAGAAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAAGTTTCCAACCGATTCT - 240
- L Q K P G Q S P K L L I Y K V S N R F S
241 - GGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGAGATTTCACACTCAAGATCAGC - 300
- G V P D R F S G S G S G T D F T L K I S
301 - AGAGTGGAGGCTGAGGATCTGGGAGTTTATTACTGCTTTCAAAGGCACACATGCTCCGTAC - 360
- R V E A E D L G V Y Y C F Q G T H A P Y
361 - ACGTTCGGAGGGGGACCAAGCTGGAATAAACTCGGGCCGCACCATCTGCTTCATC - 420
- T F G G G T K L E I K T A A A P S V F I
421 - TTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGCTGCTGAAT - 480
- F P S D E Q L K S G T A S V V C L L N
481 - AACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCCAATCGGGT - 540
- N F Y P R E A K V Q W K V D N A L Q S G
541 - AACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC - 600
- N S Q E S V T E Q D S K D S T Y S L S S
601 - ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACC - 660
- T L T L S K A D Y E K H K V Y A C E V T
661 - CATCAGGGCCTGAGCTCGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGT**TGA** (SEQ ID NO: 15)
- H Q G L S S P V T K S F N R G E C * (SEQ ID NO: 16)

Murine 6B5 variable region leader sequence

Human kappa constant region NotI restriction site **TGA** stop codon

Fig. 10

1-ATGGAATGCAGCTGTGTAATGCTCTTCTCCTCTGTCAGGAACCTGCAGGTGTCTCTCTGAG-60
 -M E C S C V M L F L L S G T A G V L S E
 61-GTCCAGCTGCAACAGTCTGGACCTGAGTTGGTGAAGCCTGGGGCTTCAGTGAAGATGTCC-120
 -V Q L Q Q S G P E L V K P G A S V K M S
 121-TGCAAGGCTTCTGGCTACACTTTCACTGACTACTACATACACTGGATGAAGCAGAGCCAT-180
 -C K A S G Y T G T D Y Y I H W M K Q S H
 181-GGAAAGAGCCTTGAGTGGATTGGATATATTTATCCTAAACAACGGTGGTAATGGCTACAAC-240
 -G K S L E W I G Y I Y P N N G G N G Y N
 241-CAGAAGTTCAAGGCAAGGCCACATTGACTGTAGACAAAGTCTCCAGCACAGCCTACATG-300
 -Q K F K G K A T L T V D K S S S T A Y M
 301-GAGCTCCGCACCCCTGACATCTGAGGACTCTGCACTTATTACTGTGGAAGATCTACCTGG-360
 -E L R T L T S E D S A V Y Y C G R S T W
 361-GACGACTTTGACTACTGGGGCCAAGGCACCACCTCTCACAGTCTCCTCAGCTAGCACCAAG-420
 -D D F D Y W G Q G T T L T V S S A S T K
 421-GGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCC-480
 -G P S V F P L A P C S R S T S E S T A A
 481-CTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAAACCGGTGACGGTGTGCGTGGAACTCAGGC-540
 -L G C L V K D Y F P E P V T V S W N S G
 541-GCTCTGACCAGCGCGGTGCACACCTTCCCAGCTGTCTCTACAGTCTCCTCAGGACTCTACTCC-600
 -A L T S G V H T F P A V L Q S S G L Y S
 601-CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAAC-660
 -L S S V V T V P S S N F G T Q T Y T C N
 661-GTAGATCACAAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTC-720
 -V D H K P S N T K V D K T V E R K C C V
 721-GAGTGCCCCACCGTGCCCCAGCACCCACCTGTGGCAGGACCGTCAGTCTTCTCTCCCCCA-780
 -E C P P C P A P P V A G P S V F L F P P

Fig. 11A

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781-AAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACGTGCGTGGTGGAC-840
-K P K D T L M I S R T P E V T C V V D
841-GTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGAGGTGCAT-900
-V S H E D P E V Q F N W Y V D G V E V H
901-AATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCCGTGTGGTCAGCGTC-960
-N A K T K P R E E Q F N S T F R V V S V
961-CTCACCGTTGTGCACCAAGGACTGGCTGAACGGCAAGGATACAAGTGCAAGGTCTCCAAC-1020
-L T V V H Q D W L N G K E Y K C K V S N
1021-AAAGGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAGGGCAGCCCCGAGAA-1080
-K G L P A P I E K T I S K T K G Q P R E
1081-CCACAGGTGTACACCCCTGCCCCCATCCCGGAGGAGATGACCAAGAACCAGGTCAGCCTG-1140
-P Q V Y T L P P S R E E M T K N Q V S L
1141-ACCTGCCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGG-1200
-T C L V K G F Y P S D I A V E W E S N G
1201-CAGCCGGAGAACAAC TACAAGACCAACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC-1260
-Q P E N N Y K T T P P M L D S D G S F F
1261-CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCGGGAACGTCTTCTCATGC-1320
-L Y S K L T V D K S R W Q Q G N V F S C
1321-TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGACCTCTCCCTGTCTCCG-1380
-S V M H E A L H N H Y T Q K S L S L S P
1381-GGTAATGA (SEQ ID NO: 17)
-G K * (SEQ ID NO: 18)

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	Murine 6B5 variable region	<u>leader sequence</u>	
	Human IgG2 constant regions	<u>NheI restriction site</u>	<u>TGA stop codon</u>

Fig. 11B

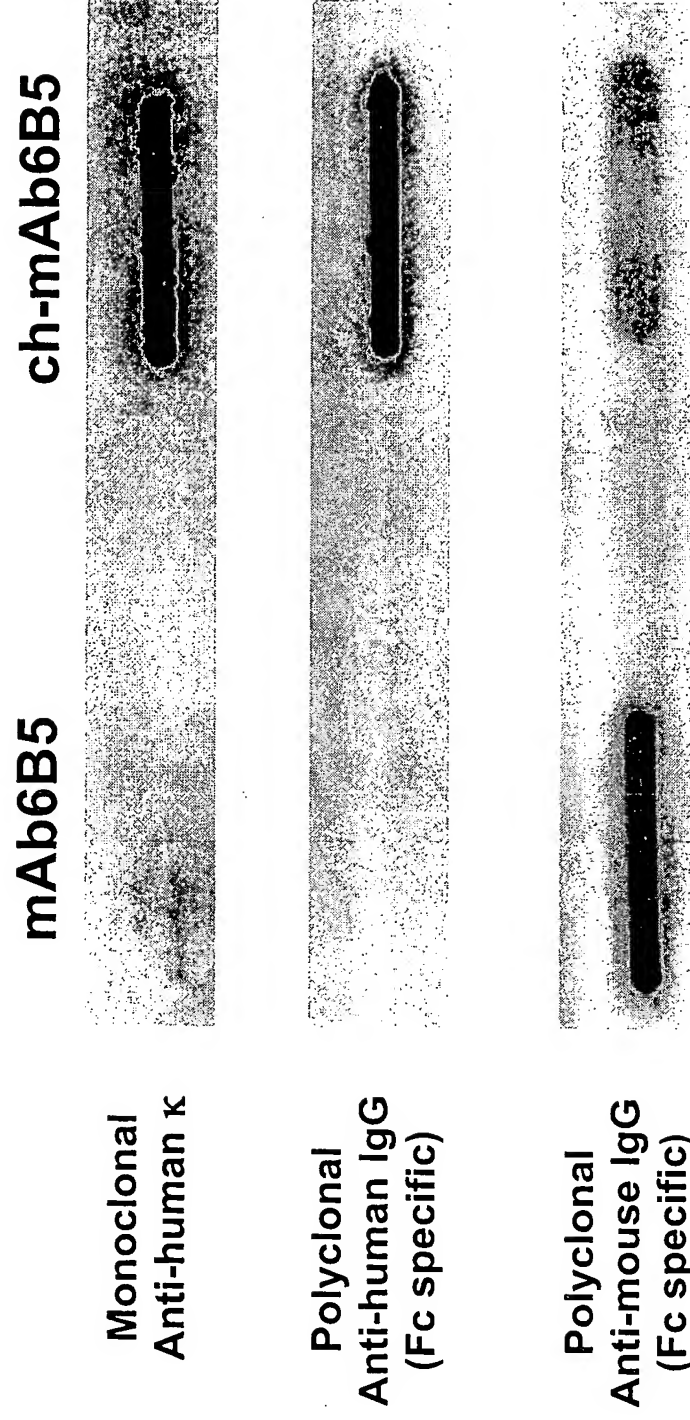


Fig. 12

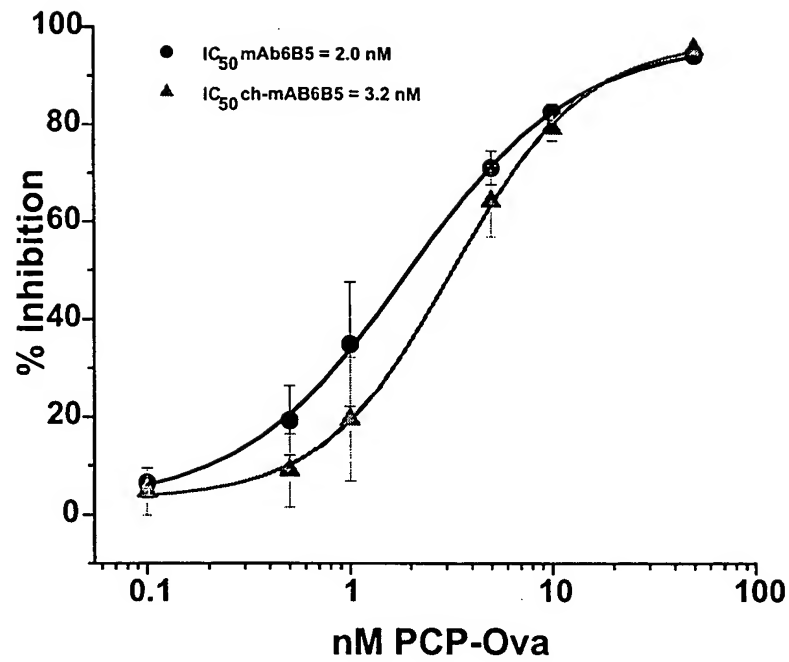


Fig. 13

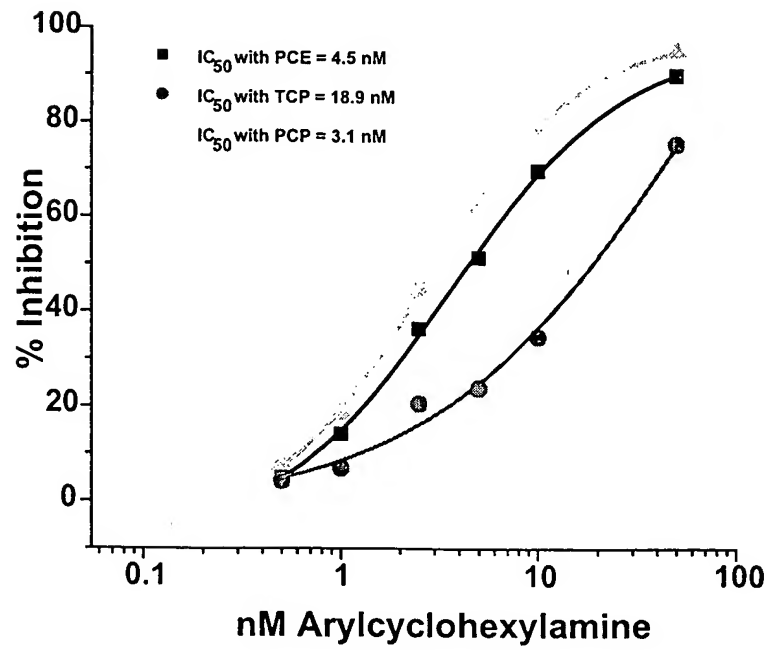


Fig. 14